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Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=1; day=23; hr=14; min=24; sec=59; ms=835;]

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Application No: 10808758 Version No: 2.0

Input Set:

Output Set:

Started: 2008-01-10 20:18:04.947
Finished: 2008-01-10 20:18:11.586
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 639 ms
Total Warnings: 118
Total Errors: 0
No. of SeqIDs Defined: 121
Actual SeqID Count: 121

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2008-01-10 20:18:04.947
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Total Warnings: 118
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Actual SeqID Count: 121

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22) This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (34)
W 402	Undefined organism found in <213> in SEQ ID (35)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (37)
W 402	Undefined organism found in <213> in SEQ ID (38)
W 402	Undefined organism found in <213> in SEQ ID (39)
W 402	Undefined organism found in <213> in SEQ ID (40)

SEQUENCE LISTING

<110> The Scripps Research Institute
Von Seggern, Daniel J.

<120> ADENOVIRUS PARTICLES WITH ENHANCED INFECTIVITY OF DENDRITIC
CELLS AND PARTICLES WITH DECREASED INFECTIVITY OF HEPATOCYTES

<130> SCRIP1860-2

<140> 10808758
<141> 2004-03-24

<150> US 60/467,500

<151> 2003-05-01

<150> US 60/459,000

<151> 2003-03-28

<160> 121

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Adenovirus type 5

<220>

<221> CDS
<222> (1)...(1743)

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1 5 10 15

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Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50 55 60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu 100	105	110	336
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr 115	120	125	384
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile 130	135	140	432
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln 145	150	155	480
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr 165	170	175	528
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu 180	185	190	576
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly 195	200	205	624
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr 210	215	220	672
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr 225	230	235	720
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala 245	250	255	768
gga gga cta agg att gat tct caa aac aca aga cgc ctt ata ctt gat gtt Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val 260	265	270	816
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln 275	280	285	864
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn 290	295	300	912
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu 305	310	315	960
		320	

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile 325	330	335	1008	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro 340	345	350	1056	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp 355	360	365	1104	
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp 370	375	380	1152	
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr 385	390	395	400	1200
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu 405	410	415	1248	
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile 420	425	430	1296	
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile 435	440	445	1344	
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn 450	455	460	1392	
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe 465	470	475	480	1440
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly 485	490	495	1488	
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala 500	505	510	1536	
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys 515	520	525	1584	
cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp 530	535	540	1632	
aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc			1680	

Thr	Thr	Pro	Ser	Ala	Tyr	Ser	Met	Ser	Phe	Ser	Trp	Asp	Trp	Ser	Gly	
545																560
cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca															1728	
His	Asn	Tyr	Ile	Asn	Glu	Ile	Phe	Ala	Thr	Ser	Ser	Tyr	Thr	Phe	Ser	
																565
570															575	
tac att gcc caa gaa taa																1746
Tyr	Ile	Ala	Gln	Glu												
																580

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 <212> PRT
 <213> Adenovirus type 5

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Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser	
																35
Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	Leu	Ala	Leu	
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Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Asn	Leu	Thr	Ser	
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Gln	Asn	Val	Thr	Thr	Val	Ser	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Ser	Asn	
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Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu	
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Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr	
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Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile	
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Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln	
145																150
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr	
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Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu	
																180
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly	
																195
Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr	
																210
Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr	
225																230
Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu	Asn	Val	Ala	
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Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile	Leu	Asp	Val	
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Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Asn	Gln	Leu	Asn	Leu	Arg	Leu	Gly	Gln	
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Gly	Pro	Leu	Phe	Ile	Asn	Ser	Ala	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn	
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Lys	Gly	Leu	Tyr	Leu	Phe	Thr	Ala	Ser	Asn	Asn	Ser	Lys	Lys	Leu	Glu	

305	310	315	320
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			
	325	330	335
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro			
	340	345	350
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp			
	355	360	365
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp			
	370	375	380
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr			
	385	390	395
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu			
	405	410	415
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile			
	420	425	430
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile			
	435	440	445
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn			
	450	455	460
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe			
	465	470	475
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly			
	485	490	495
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala			
	500	505	510
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys			
	515	520	525
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp			
	530	535	540
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly			
	545	550	555
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser			
	565	570	575
Tyr Ile Ala Gln Glu			
	580		

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<211> 1746
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> CDS
<222> (1) ... (1743)

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Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20 25 30

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Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser			
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ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc			192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu			
50	55	60	
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc			240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser			
65	70	75	80
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac			288
Gln Asn Val Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn			
85	90	95	
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta			336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu			
100	105	110	
act gtg gct gcc gca cct cta atg gtc gcg ggc aac aca ctc acc			384
Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr			
115	120	125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att			432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile			
130	135	140	
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa			480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln			
145	150	155	160
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act			528
Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr			
165	170	175	
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg			576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu			
180	185	190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg			624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly			
195	200	205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act			672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr			
210	215	220	
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Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr			
225	230	235	240
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245	250	255	

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt		816	
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260	265	270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag		864	
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln			
275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac		912	
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			
290	295	300	
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Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			
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gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata		1008	
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			
325	330	335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca		1056	
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro			
340	345	350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat		1104	
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp			
355	360	365	
tca aac aag gct atg cct aaa cta gga act ggc ctt agt ttt gac		1152	
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp			
370	375	380	
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act		1200	
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr			
385	390	395	400
ttg tgg acc aca cca gct cca gag gct aac tgt aga cta aat gca gag		1248	
Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu			
405			